

0;sd

Db 121 AGTCATTCGCTGACCTGATTCACCAATGACGATGCTACATCTTGGCAAGAAATTTGAA 180
Oy 181 TTGAAGATCATTTTGAAGAAACATGGAGCAAAATTTGGTGTCTGAAGTGGCTTCTAAAC 240
Db 181 TTGAAGACATTTTGAAGAAATTTGGTGTCTGAAGTGGCTTCTAAAC 240
Oy 241 AATGATATTCGCTGATGGAGCACTACGCAAGTTTGAAGCAAGTGGCTTCTAAAC 300
Db 241 AATGATATTCGCTGATGGAGCACTACGCAAGTTTGAAGCAAGTGGCTTCTAAAC 300
Oy 301 GAAGACATTTTGAAGAAATTTGGTGTCTGAAGTGGCTTCTAAAC 360
Db 301 GAAGACATTTTGAAGAAATTTGGTGTCTGAAGTGGCTTCTAAAC 360
Oy 361 ACAGCAACGACAGCTGTGAGCTTGAAGCAAGTGGCTTCTAAAC 420
Db 361 ACAGCAACGACAGCTGTGAGCTTGAAGCAAGTGGCTTCTAAAC 420
Oy 421 GAAGCTATTCGCTGATGGAGCACTACGCAAGTTTGAAGCAAGTGGCTTCTAAAC 480
Db 421 GAAGCTATTCGCTGATGGAGCACTACGCAAGTTTGAAGCAAGTGGCTTCTAAAC 480
Oy 481 TCAGAACTATGGAGCTGTGGCAAGTGGCTTGAAGCAAGTGGCTTCTAAAC 540
Db 481 TCAGAACTATGGAGCTGTGGCAAGTGGCTTGAAGCAAGTGGCTTCTAAAC 540
Oy 541 ATGGAACAGAACTGAAAGTGGTGAAGCACTTGAAGCAAGTGGCTTCTAAAC 600
Db 541 ATGGAACAGAACTGAAAGTGGTGAAGCACTTGAAGCAAGTGGCTTCTAAAC 600
Oy 601 TACATGCTACAGACATGAAAGTGGTGAAGCACTTGAAGCAAGTGGCTTCTAAAC 660
Db 601 TACATGCTACAGACATGAAAGTGGTGAAGCACTTGAAGCAAGTGGCTTCTAAAC 660
Oy 661 AGGATATTTGAAGAAATTTGGTGTCTGAAGTGGCTTGAAGCAAGTGGCTTCTAAAC 720
Db 661 AGGATATTTGAAGAAATTTGGTGTCTGAAGTGGCTTGAAGCAAGTGGCTTCTAAAC 720
Oy 721 ACCACGCTCATTTACTCATTTTGAAGCAAGTGGCTTGAAGCAAGTGGCTTCTAAAC 780
Db 721 ACCACGCTCATTTACTCATTTTGAAGCAAGTGGCTTGAAGCAAGTGGCTTCTAAAC 780
Oy 781 GTCTTGAAGCAAGTGGTGTCTGAAGCAAGTGGCTTGAAGCAAGTGGCTTCTAAAC 840
Db 781 GTCTTGAAGCAAGTGGTGTCTGAAGCAAGTGGCTTGAAGCAAGTGGCTTCTAAAC 840
Oy 841 GATCGTCTTGAAGCAAGTGGTGTCTGAAGCAAGTGGCTTGAAGCAAGTGGCTTCTAAAC 900
Db 841 GATCGTCTTGAAGCAAGTGGTGTCTGAAGCAAGTGGCTTGAAGCAAGTGGCTTCTAAAC 900
Oy 901 GAAGATCTAGGACATGAAATTTGAAGCAAGTGGTGTCTGAAGCAAGTGGCTTCTAAAC 960
Db 901 GAAGATCTAGGACATGAAATTTGAAGCAAGTGGTGTCTGAAGCAAGTGGCTTCTAAAC 960
Oy 961 ATTACAGTGTATTAAGTGAAGCAAGTGGTGTCTGAAGCAAGTGGCTTCTAAAC 1020
Db 961 ATTACAGTGTATTAAGTGAAGCAAGTGGTGTCTGAAGCAAGTGGCTTCTAAAC 1020
Oy 1021 GCTAACGCTATTCGATTTAAATTCGCAATTTGAAGCAAGTGGCTTCTAAAC 1080
Db 1021 GCTAACGCTATTCGATTTAAATTCGCAATTTGAAGCAAGTGGCTTCTAAAC 1080
Oy 1081 GAAAAATCTACAGAACTTTGGCAAAATTTAGCTGTGTGATCTTTATCAAAAGTGA 1140
Db 1081 GAAAAATCTACAGAACTTTGGCAAAATTTAGCTGTGTGATCTTTATCAAAAGTGA 1140
Oy 1141 GCTCCACAGACAGCTTTAAAGAAATTTGCAATTTGCAATTTGCAATTTGCAATTTGCA 1200
Db 1141 GCTCCACAGACAGCTTTAAAGAAATTTGCAATTTGCAATTTGCAATTTGCAATTTGCA 1200
Oy 1201 ACAGCTGACGCTGTGAAGAAATTTGCTGTGTGTGTAACACCACTTTATACGCTT 1260
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Db 1201 ACTGCTGACCTGTGTAAGAAATTTGAGAGTGTGGAACAGCTTTGCCAATGTC 1260
Oy 1261 ATTGAAATATGACAGCTTCTGAGCTTGAAGCAAGTGGTGTCTGAAGTGGCTTCTAAAC 1320
Db 1261 ATTGAAATATGACAGCTTCTGAGCTTGAAGCAAGTGGTGTCTGAAGTGGCTTCTAAAC 1320
Oy 1321 CTGCTGCTGTGAAGAGCTGTGACGTAATTTGCTTAAATGCTGTGAGAGGCTTCC 1380
Db 1321 CTGCTGCTGTGAAGAGCTGTGACGTAATTTGCTTAAATGCTGTGAGAGGCTTCC 1380
Oy 1381 GTATTTATGACAGCTTGAAGAAATTTGAGCAAGTGGTGTGTAACAGTGTGCAACAGT 1440
Db 1381 GTATTTATGACAGCTTGAAGAAATTTGAGCAAGTGGTGTGTAACAGTGTGCAACAGT 1440
Oy 1441 GATGCTGTGATGATTTAAACAGAAATTTGAGCAAGTGGTGTGTAACAGTGTGCAACAGT 1500
Db 1441 GATGCTGTGATGATTTAAACAGAAATTTGAGCAAGTGGTGTGTAACAGTGTGCAACAGT 1500
Oy 1501 CTGCAAAATGCAAGCTTCTGAGTGTGTAATTTTGAAGCAAGTGGTGTGTAAT 1560
Db 1501 CTGCAAAATGCAAGCTTCTGAGTGTGTAATTTTGAAGCAAGTGGTGTGTAAT 1560
Oy 1561 AATCCTGAACAGCTGACGCTGACGCAAGTGGTGTGTAACAGTGGTGTGTAACAGT 1620
Db 1561 AATCCTGAACAGCTGACGCTGACGCAAGTGGTGTGTAACAGTGGTGTGTAACAGT 1620
Oy 1621 GGTG 1624
Db 1621 GGTG 1624
RESULT 2
US-09-070-927A-42
Sequence 42, Application US/09070927A
Patent No. US200201161
GENERAL INFORMATION:
APPLICANT: Charles A. Kunsch
Patrick J. Dillon
Steven Barash
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 982
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 Inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,927A
FILING DATE: 04-May-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/046,655
FILING DATE: 1997-05-16
APPLICATION NUMBER: 60/044,031
FILING DATE: 1997-05-06
APPLICATION NUMBER: 60/066,009
FILING DATE: 1997-11-14
ATTORNEY/AGENT INFORMATION:
NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB369
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SBO ID NO: 42:
SEQUENCE CHARACTERISTICS:

LENGTH: 3625 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 42:
 US-09-070-927A-42

Query Match 57.5% Score 942.6; DB 10; Length 3625;
 Best Local Similarity 74.2%; Pred. No. 1.3e-220;
 Matches 1191; Conservative 0; Mismatches 415; Indels 0; Gaps 0;

QY 1 ATGCCAAGAAATCAATTTTCAGCAGATGCGGCTGCTCCATGGTCCGCGAGTTGAT 60
 DB 364 ATGCCAAGAAATCAATTTTCAGCAGATGCGGCTGCTCCATGGTCCGCGAGTTGAT 423
 QY 61 ATGTACAGATACCGTCAGATTAACGCTTGGCTTAAAGGCGCAATGTTCTTGA 120
 DB 424 ATGTACAGATACCGTCAGATTAACGCTTGGCTTAAAGGCGCAATGTTCTTGA 483
 QY 121 AAAGCTTGTCTCCCTTAATTAATGACGGGTAACCTTGGCTTAAAGGCGCAATGTTCTTGA 180
 DB 484 AAAGCTTGTCTCCCTTAATTAATGACGGGTAACCTTGGCTTAAAGGCGCAATGTTCTTGA 543
 QY 181 TTAGAAATCATTTTGAAGCAATGAGCAAAATTTGCTGCAAGGCTTAAAGGCGCAATGTTCTTGA 240
 DB 544 TTAGAAATCATTTTGAAGCAATGAGCAAAATTTGCTGCAAGGCTTAAAGGCGCAATGTTCTTGA 603
 QY 241 AATGATATGCTGCTGATGAGGAGCACTACTGCAACAGTTTTCACCAAGCCATTTTCAT 300
 DB 604 AATGATATGCTGCTGATGAGGAGCACTACTGCAACAGTTTTCACCAAGCCATTTTCAT 663
 QY 301 GAAAGCACTAAAATATGACAGCAGGCTGTAATCAATTTGGTATCCGTCGAGGCAATGTA 360
 DB 664 GAAAGCACTAAAATATGACAGCAGGCTGTAATCAATTTGGTATCCGTCGAGGCAATGTA 723
 QY 361 ACAGCAACAGCAACAGCTGTGAAAGCTTGAAGCCATTTGCTCAACGCTATCTGGCAAG 420
 DB 724 TTACCAACCAAAAACAGCAGTAGAAGATTAACCAATTTTCATCTGTAAGTTGATCAAAA 783
 QY 421 GAACCTATTTGCTCAGGCTGCTGAGATATCATCAGCTGGAAGAAAGTTGAGAGATATCA 480
 DB 784 GAACCTATTTGCTCAGGCTGCTGAGATATCATCAGCTGGAAGAAAGTTGAGAGATATCA 843
 QY 481 TCAGCACTATGAGGCTGTGGGCAACAGTGTGTGATTAACATGCAAGAAATGTCAGCT 540
 DB 844 GCGATGCAATGCAAAAAGTTGTAACGCGCTAATTTACATTTGAAGATTAAGAGG 903
 QY 541 ATGGAACAGCACTGAAGTGTGTAAGGCAATTTGACACCTGGTTACTGTTCTCAA 600
 DB 904 ATGGAACAGCACTGAAGTGTGTAAGGCAATTTGACACCTGGTTACTGTTCTCAA 963
 QY 601 TACATGCTACAGCAATGAAAAATGGTTCAGACCTTGAAGAAAGCCATTATCTTAATC 660
 DB 964 TACATGCTACAGCAATGAAAAATGGTTCAGACCTTGAAGAAAGCCATTATCTTAATC 1023
 QY 661 ACGGATTAAGAGTGTCAACATCCAGACATTTTGCACACTGTGAGAGGTTCTTAA 720
 DB 1024 ACGGATTAAGAGTGTCAACATCCAGACATTTTGCACACTGTGAGAGGTTCTTAA 1083
 QY 721 ACCAAGCGTCACTATGATATTAATGCAATGATGATGATGATGATGATGATGATGATGAT 780
 DB 1084 ACCAAGCGTCACTATGATATTAATGCAATGATGATGATGATGATGATGATGATGATGAT 1143
 QY 781 GTCCTAAGAGATTCGTGATCTTCAATGATGATGATGATGATGATGATGATGATGATGAT 840
 DB 1144 GTCCTAAGAGATTCGTGATCTTCAATGATGATGATGATGATGATGATGATGATGATGAT 1203
 QY 841 GATGCTGTAAAGTATGCTGAAGACATGCTATCTTGAAGAGTGTGATGATGATGATGATGAT 900
 DB 1204 GATGCTGTAAAGTATGCTGAAGACATGCTATCTTGAAGAGTGTGATGATGATGATGATGAT 1263
 QY 901 GAGATCTAGGACTTGAATTAAGATGCTACATGACAGCCCTTGGACAGGCTCTAG 960

DB 1264 GAGACTTAGGCTAGAGTTAAAGACACACTATTGAAGAACTTGAAGAAATGCTAGCAA 1323
 QY 961 ATTACAGTTGATAAAGATAGCAGACTAATTTGTAAGGTTCCAGAAAGTTCAGAACTAT 1020
 DB 1324 GTAGTGTGAGCAAGATTAACACAACTATGTAAGGTTGCTGTTCAAAAAGCACTT 1383
 QY 1021 GCTAACGCTATTGCTGATTAATATCGCAATTTGAAGCAACAACTTCTGATGATGATGAT 1080
 DB 1384 GATGCGCCGCTGCTAATTAATTAAGCAAAATCGCGAAACAACTGCTGATTTGATGCT 1443
 QY 1081 GAAATATACAGAGGTTGGCGAAATATGCTGCTGATGATGATGATGATGATGATGATGAT 1140
 DB 1444 GAAATATACAGAGGTTGATTAATTAAGCAAAATCGCGAAACAACTGCTGATTTGATGCT 1503
 QY 1141 GCTCAACAGAGGCTGATTAAGAAATTAAGAAATTAAGAAATTAAGAAATTAAGAAATTAAG 1200
 DB 1504 GCTCAACAGAGGCTGATTAAGAAATTAAGAAATTAAGAAATTAAGAAATTAAGAAATTAAG 1563
 QY 1201 ACAGCTGAGCGCTGTAAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
 DB 1564 ACAGCTGAGCGCTGTAAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1623
 QY 1261 ATTGAAGATGACAGCTTTGACCTTGAAGGCGATGATGCTACTGAGCAATGATG 1320
 DB 1624 ATTGAAGATGACAGCTTTGACCTTGAAGGCGATGATGCTACTGAGCAATGATG 1683
 QY 1321 CTTCGCTGCTAGAGAGGCTGTAGCTCAAAATTTGCTTAATGCTGGTACGAGGCTGC 1380
 DB 1684 CTTCGCTGCTAGAGAGGCTGTAGCTCAAAATTTGCTTAATGCTGGTACGAGGCTGC 1743
 QY 1381 GTAGTTATGCAAGGTTGAAAGACGCTGCGAGACAGAGATTTAATCTGCAAGCT 1440
 DB 1744 GTAGTTATGCAAGGTTGAAAGACGCTGCGAGACAGAGATTTAATCTGCAAGCT 1803
 QY 1441 GATGAGGTTGATGATTAAGAAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1500
 DB 1804 GATGAGGTTGATGATTAAGAAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1863
 QY 1501 CTTCGAATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
 DB 1864 CTTCGAATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1923
 QY 1561 AAACCTGACACGCTACGCGCAGCCGCAATGCTGCAAGGATGAG 1606
 DB 1924 AAACCTGACACGCTACGCGCAGCCGCAATGCTGCAAGGATGAG 1969

RESULT 3
 US-09-790-988-1
 : Sequence 1, Application US/09790988
 : Patent No. US20020127687A1
 : GENERAL INFORMATION:
 : APPLICANT: SHIGENOBU, SHUJI
 : APPLICANT: MATSUNABE, HIDEKI
 : APPLICANT: SAKAKI, YOSHITOKI
 : APPLICANT: MATSUNABE, HIDEKI
 : TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
 : FILE REFERENCE: 081356/0159
 : CURRENT APPLICATION NUMBER: US/09/790, 988
 : PRIOR FILING DATE: 2001-02-23
 : PRIOR APPLICATION NUMBER: JP2000-107160
 : NUMBER OF SEQ ID NOS: 7
 : SOFTWARE: PatentIn Ver. 2.1
 : SEQ ID NO 1
 : LENGTH: 640681
 : TYPE: DNA
 : ORGANISM: Buchnera sp.
 : US-09-790-988-1

Query Match 37.6% Score 615.8; DB 10; Length 640681;
 Best Local Similarity 62.8%; Pred. No. 2.1e-139;
 Matches 931; Conservative 0; Mismatches 582; Indels 6; Gaps 2;


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Db 658 GAAGACAGTTCGAAATATGGGTGGCGAGATGTGGAAGAAGTTCCTTAAGCAAC 717
Oy 244 GATATTGCTGATGGAGACACTACTGACAGATTTTGACACAGCCATTTGTCATGAA 303
Db 718 GACCTGCGAGCGGATACCAACACCTACTGCTAGGCTATATCATCTGAA 777
Oy 304 GGACGTAAAAATGTGACAGAGTGTCAATTCATATGCTTCGAGCATTTGAACA 363
Db 778 GGTCTGAAGACCTTGTCTGGCGGATGAAACCCGATGACCTGAAAGGTGATGACAAA 837
Oy 364 GCACACGACACACTTGTGAAGCCTTGAAGCCATTTGCTCAACCTGTATCTGACAGAA 423
Db 838 GCGGTTCACCTGCTGATGAAGACTGAAGAGCGGTGCTACACTGCTGACATCTGAAA 897
Oy 424 GCTATTGCTAGTGTGCTGACATCATCAGCTC---TGAAAAATTGAGAGATATATC 480
Db 898 GCGATTGCTAGTGTGCTGACATCATCAGCTC---TGAAAAATTGAGAGATATATC 957
Oy 481 TCAGAGCTATGAGAGGTGTGGGACAGATGTGATATCATCTGAGAGATATCTCAAGT 540
Db 958 GCTGAAGCGATGACAAAGTCGTTAAAGAGCGCTTACCGTTGAAGACGGTACCGGT 1017
Oy 541 ATGGAACAGAACTTGAAGTGTGAAGGATGCAATTTGACGTTGCTGCTCA 600
Db 1018 CTGACAGCACTGAGCTGTGAAGGTATGCAAGTTCGACCGTGTCTACTCTCTCT 1077
Oy 601 TCACTGCTCAGACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660
Db 1078 TACTTCATCAACAGCGGAACTGGCGGATGATGATGATGATGATGATGATGATG 1137
Oy 661 ACAGTAAAAAGTGTCAACATCAGACATTTTGGCACTTACTGAGAGATTTCTTAA 720
Db 1138 GCTGACAGAAATCTCCAACTCCGCAAAATGCTGCGGATTTCTGAAAGCTGTGGCAA 1197
Oy 721 ACCAACGCTCATTCATATATGATGATGATGATGATGATGATGATGATGATGATG 780
Db 1198 GAGGCAAAACCGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 1257
Oy 781 GCTTTGACAAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 840
Db 1258 GTTGTAAACCACTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 1317
Oy 841 GATGCTGTAAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 900
Db 1318 GATGCTGTAAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1377
Oy 901 GAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 960
Db 1378 GAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1437
Oy 961 ATTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1020
Db 1438 GTTGTAAACCACTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 1497
Oy 1021 GCTAACGTAATGCACTGATTAATGCAATTTGAACAAACAACTTGTGACTTGAACGT 1080
Db 1498 CAGGCGGTGTGCTCAGATCCCTCAGCAAGATGTAAGAAAGCAATCTGACTGACGCT 1557
Oy 1081 GAAAACTACAGAACTTTGGCAATTTAGCTGTTGTTGATCAAGATGAA 1140
Db 1558 GAAAACTACAGAACTTTGGCAATTTAGCTGTTGTTGATCAAGATGAA 1617
Oy 1141 GCTCAACAGAGAGCTTTAAAGAAATGAATTCCTGATGAGATGATGATGATGATGATG 1200
Db 1618 GCTCAACAGAGAGCTTTAAAGAAATGAATTCCTGATGAGATGATGATGATGATGATG 1677
Oy 1201 ACAGTGAACCGCTTGAAGAGATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
Db 1678 ACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1737
Oy 1261 ATTGAAGATGACGCTTTGAGCTTGAAGGCGATGATGATGATGATGATGATGATGATG 1317
Db 1738 GCGCTTAACCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1797

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Oy 1318 GTCTCTGCTCTAGAAAGCTCTAGCTCAATTTGCTTTAATGCTGGTACAGGC 1377
Db 1798 GCACTGCGAATGAGAGCTCCGCTGCTGATGATGATGATGATGATGATGATGATGATG 1857
Oy 1378 TCGGATGATTAAGCAAGTTGAAGAAACAGCCCTGACAGAACAGATTTAATGCTCAACA 1437
Db 1858 TCTGTTGTTGCTAACCGTTAAAGCGCGGACGCGCACTAGGTTCAACACAGCAAC 1917
Oy 1438 GGTGAGTGGTTGATGATTAAGACAGATCATTTGACCCCTGCAAGATGACAGATCA 1497
Db 1918 GAAGAAATACGCAACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1977
Oy 1498 GCGCTCAAAATGAGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1557
Db 1978 GCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2037
Oy 1558 AATAAAGCTGACAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1606
Db 2038 GACCTGCGAAGAAACGATGATGATGATGATGATGATGATGATGATGATGATGATG 2086

RESULT 5
US-09-841-132-380
Sequence 380, Application US/09841132
Patent No. US20020061848A1
GENERAL INFORMATION:
APPLICANT: Bhalla, Ajay
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
FILE REFERENCE: 210121.469C8
CURRENT FILING DATE: 2001-04-23
NUMBER OF SEQ ID NOS: 599
SOFTWARE: FastSeq for Windows Version 3.0/4.0
SEQ ID NO 380
LENGTH: 1635
TYPE: DNA
ORGANISM: Chlamydia pneumoniae
US-09-841-132-380

Query Match 32.4%, Score 530.4, DB 10, Length 1635,
Best Local Similarity 59.5%, Pred. No. 7e-120,
Matches 957, Conservative 0, Mismatches 636, Indels 15, Gaps 3;

Oy 4 GCAAAAGAAATCAATTTTCACAGATGCGCGTGTGCTGCCATGCTGCGGAGTGTGATG 63
Db 7 GCGAAATATTAATTAATTAATGAGAGCAAGAAATTAATTAATTAATTAATTAATTAAT 66
Oy 64 TTAGCAGATACCGTCAAAAGTAAAGCTGTGCTTAAGAGGCGCAATGTTGTTGTAATAA 123
Db 67 CTGCGAAGCAGTAATAAGTACTGTAGTCTTAAGAGGCTGACGTAGTATGATTAAG 126
Oy 124 GCTTTGCTGCTCTTAATTAATTAATGAGAGGCTTAACCTGCTTAAGATGATTA 183
Db 127 ACCTTTGCTGCTCTTAATTAATTAATGAGAGGCTTAACCTGCTTAAGATGATTA 186
Oy 184 GAAGATCATTTTGAAGAACTGAGAGCAAAATTTGCTGATGATGATGATGATGATGATG 243
Db 187 GAAGATCATTTTGAAGAACTGAGAGCAAAATTTGCTGATGATGATGATGATGATGATG 246
Oy 244 GATATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 303
Db 247 GATATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 306
Oy 304 GCACTTAATAATGATGACAGAGTGTGATGATGATGATGATGATGATGATGATGATGATG 363
Db 307 GCTTAATAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 366
Oy 364 GCACAGCAACAGCTGTTGAAGCTTGAAGCAATTTGCTCAACCTGATCTGCGAAGAA 423

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Db 367 GCCGTAAAGTTGTTGATGACGCAAAAAATAGTAACCTGTACAACTACAAA 426
OY 424 GCTATGCTCAGGTCGTCGATGATCATGACGCTCTGA---AAAGTTGGAGATATTC 480
Db 427 GAAATGCTCAAGTAGTACTATCTACGAAATATGATTCGGAATCGAATCTTAT 486
OY 481 TCAGAGCTATGAGCGGTGGGCAACGATGCTGTACATACATGGAAGATTCGAGT 540
Db 487 GCAGAGCTATGGAAGAGTGTGTAAGAGATCCCTTCCTGCTGTTGGAAGGC 546
OY 541 ATGGAAGAGAGCTGAGAGTGTGTAAGAGATCCCTTCCTGCTGTTGGAAGGC 600
Db 547 TTGGAAGAGAGCTGAGAGTGTGTAAGAGATCCCTTCCTGCTGTTGGAAGGC 606
OY 601 TACATGCTCAGACATGAAATAATGCTGACACCTGGAACCCATTATCTTAATC 660
Db 607 TACATGCTCAGACATGAAATAATGCTGACACCTGGAACCCATTATCTTAATC 666
OY 661 ACGATTAAGAGAGTGTGTAAGAGATCCCTTCCTGCTGTTGGAAGGC 720
Db 667 TACATGCTCAGACATGAAATAATGCTGACACCTGGAACCCATTATCTTAATC 726
OY 721 ACGAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 780
Db 727 TCTGAGACCCCTCTTTTATCATGCAAGAAATGGAAGAGAGCTTACGACCTA 786
OY 781 GTCGTGACAGATGCTGATGATGATGATGATGATGATGATGATGATGATGATG 840
Db 787 GTAGTCAATGACCTCGTCGAGATTCAGAGTGTGAGTGAAGAGCTTCTGCTGCT 846
OY 841 GATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 900
Db 847 GATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 906
OY 901 GATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 960
Db 907 GATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 966
OY 961 ATTACAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1020
Db 967 GTTATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1026
OY 1021 GCTAACGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1080
Db 1027 CAAGCTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1086
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Db 1087 GAAAACTACAAAGAGCTGTCGAAATGATGATGATGATGATGATGATGATGATG 1146
OY 1141 GCTCAAGAGAGAGCTGTCGAAATGATGATGATGATGATGATGATGATGATG 1200
Db 1147 GCTCAAGAGAGAGCTGTCGAAATGATGATGATGATGATGATGATGATGATG 1206
OY 1201 ACGAGTGCAGAGCTGTCGAAATGATGATGATGATGATGATGATGATGATG 1260
Db 1207 ACGAGTGCAGAGCTGTCGAAATGATGATGATGATGATGATGATGATGATG 1266
OY 1261 ATTGAAGAGAGAGCTGTCGAAATGATGATGATGATGATGATGATGATGATG 1320
Db 1267 ATTGAAGAGAGAGCTGTCGAAATGATGATGATGATGATGATGATGATGATG 1326
OY 1312 ACGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1371
Db 1317 ACGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1386
OY 1372 GAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1431
Db 1387 GAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1446
OY 1432 GCAAGAGTGCAGAGCTGTCGAAATGATGATGATGATGATGATGATGATGATG 1491
Db 1447 TTACGTGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1506

OY 1492 CATTACAGCTCTCAAAATGACAGCTTCTGATGATGATGATGATGATGATGATGATG 1551
Db 1507 CATTACAGCTCTCAAAATGACAGCTTCTGATGATGATGATGATGATGATGATGATG 1566
OY 1552 GTTCTAATTAACCTGAA---CGAGTACGAGAGAGAGAGAGAGAGAGAGAGAG 1596
Db 1567 ATCGCTGATATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1614

RESULT 6
US-08-781-986A-266
Sequence 266, Application US/08781986A
Publicaton No. US20030054436A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248BP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8512
FAX: (301) 309-8512
INFORMATION FOR SEQ. ID NO.: 266:
SEQUENCE CHARACTERISTICS:
LENGTH: 1017 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-781-986A-266

Query Match 29.5%; Score 483.6; DB 7; Length 1017;
Best Local Similarity 67.2%; Pred. No. 1,5e-108;
Matches 681; Conservative 2; Mismatches 331; Indels 0; Gaps 0;


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OY 781 GCTTGAACAGATGCGTGGTCAATGTTGCTGCTCAAGGCCAGATTTGCT 840
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 781 GTCTCAACAGATCCGGGACCTTCAAGTCGTCGGCTTAAGCTCCCGCTTGGC 840
OY 841 GATGCTGTAAGCTATCTTGAACACATCTTCTTACAGTGGTACAGTATCA 900
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 841 GACCGCCGCAAGGCGATGCTGCAAGTATGCGCATCTTCAAGCGGTATCAAC 900
OY 901 GAGATCTAGACCTGAATTAAGATCTCAATGACACCCCTTGACAGGCTCTAA 960
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 901 GAAGAGTGGGCTGACGCTGAGGAACCCGACCTGCTGCTAGCAGCGCCGCAAG 960
OY 961 ATTACAGTTGATTAAGATAGCACAGTATTTGTAAGTTGAGAGTTCAGAGCTATT 1020
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 961 GTCTGATCCACCAAGACAGACCAACATCTGTCAGCGCGCGCTGACACCGCATC 1020
OY 1021 GCTAACGCTATTCAGTATTAATCGCAATTAGAAACAACATCTGATGACCTG 1080
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1021 GCCGAGAGTGGCCCGCATCCGCCAGAGATGAGAACAGAGCTCGATACAGACCT 1080
OY 1081 GAAGAACTCAAGAACGTTGGGAAATTAGCTGCTGCTGATAGCTTAAAGTATGA 1140
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1081 GAGAAGCTCAGAGAGCGGCTGCGCAAGCTGCGCTGCTGCTGATCAAGCGCGCT 1140
OY 1141 GCTCAACAGACAGCTTAAAGAAATGAACTTCGATTTGAGATGCTCTAAATGCT 1200
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1141 GCGGCTCAGAGCTCAACTCAAGAGCGCAAGCACCGCATGAGATGCGGCTCGCAT 1200
OY 1201 ACAGCTGACGCGCTTGAAGAGATTCCTGCTGCTGCTGAGACAGCACTTATACGCTT 1260
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1201 GCCAGGCGCGCTGAGAGGAGCATCTCCCGGAGGAGGCTGATGACCTTTGACACCG 1260
OY 1261 ATTGAAAGATAGCAGCTTTGAGGCGATGATGCTACTGACAGCTAATTTGCTG 1320
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1261 GCCCGACCCCTGAGAGCTGAAAGCTCGAAGCGCAGAGGCGACCGGCAATCTGCTG 1320
OY 1321 CTTCGCTCTAGAAAGAGCTGATGCTAATTTGCTTAAATGCTGAGTACGAGGCTCC 1380
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1321 AAGGTGCGCTGAGAGCGCGCTGAAAGATGAGCTTCACTCGGGGCTGAGGCGGCG 1380
OY 1381 GTAGTATTGACAGTGTGAAGAAACAGCCCTGACAGAACAGATTAATGCTGCAAGCT 1440
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1381 GTGCTGCGCGAGAAAGTGGCGAACTGCGGCTGCGCACAGCATGAACTGACAGCGCT 1440
OY 1441 GAGTGGTGAATGATTAAGACAGAAATCATGACCCCTGCAAGTACAGATACAGC 1500
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1441 GTCTAGAGAGTCTGCTGCTGCGGCTGCTGCTGACCGGCTCAAGTACAGCTGCTG 1500
OY 1501 CTTCAGAAAGCAGCTTCTGATGCTTATTTTGAACAACAGAGCTTTGCTTAAT 1560
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1501 CTGAGAAATGCGGCTCATCTCGGGGCTGCTCTGTAACCCAGAGCGCTGCTGCGAC 1560
OY 1561 AAACCTGAA 1569
    ||| ||| |||
DB 1561 AAGCCGGA 1569
    ||| ||| |||

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RESULT 9
US-10-267-311-3
; Sequence 3, Application US/10267311
; Publication No. US20030050469A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizer, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; PRIOR APPLICATION NUMBER: 2002-10-09
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757

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; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1623
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
; NAME/KEY: CDS
; LOCATION: (1)...(1620)
US-10-267-311-3

Query Match      28.0% Score 458.6; DB 9; Length 1623;
Best Local Similarity 55.8%; Pred No 2.6e-102;
Matches 875; Conservative 0; Mismatches 694; Indels 0; Gaps 0;

OY 1 ATGGCAAAAGAAATCAAAATTTTCACGACGATCGCGTCTCCATGCTGCGCGGATGAT 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1 ATGGCAAAAGAAATTTGCTACGACGAGAGAGGCCGCTCGCGCTGAGAGGCTTGAAC 60
OY 61 ATGTTAGCATACGCTCAAGTAAAGCTTGTCTTAAAGGCGCAATGTTCTTGA 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 61 GCCCTCCGCTACCGGTAAAGTGAATTTGGCCCAAGGCGCGCAAGCTGCTCTGGA 120
OY 121 AAAGCTTTGTTCTCCCTTATTAATGACGAGGCTTAACATTTGCTAAAGAGATGAA 180
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 121 AAGAAATGGGGTCCCGCCACATCACCAAGATGGTGTCTCATGCCCAAGAGATGAG 180
OY 181 TTGAGATATCTTTGAAACATGAGGCAAAATTTGCTGCTGTAAGTGGCTTAAAGC 240
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 181 CTGAGAGATCTTGAAGAGATGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
OY 241 AATGATTTGCTGATGAGGAGTACTGACAGCTTTTGACAAAGCCATTTGCTAT 300
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 241 GATGACGCTCCGCTGAGAGAGATGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTG 300
OY 301 GAGGATTAATAAATGTGACAGCAGTGTATCAATTTGCTGCTGAGCATTTGA 360
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 301 GAGGCTCTGCTGAGCTGCGGCGGCGCAACCCGCTGCTGCTGCTGCTGCTGCTG 360
OY 361 ACAGCAACAGCAAGCTGTGAAAGCTTTGAAAGCCATTGCTCAACTGTATCTGCAAG 420
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 361 AAGGCTGTGAGAGAGTCAACGAGACCTGCTCAAGGCGCGCAAGAGAGTGAAGCAAG 420
OY 421 GAAGCTATTGCTCAGGCTGCTGCAATATCATCAGCTGTGAAAGATTTGAGATATC 480
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 421 GAGCAGATTCGCGCCACCGCAGGATTTTGGGGGTGACCACTGCTGCTGCTGCTG 480
OY 481 TCAGAGCTATGAGAGCTGTGAGCAAGCATGATGATTTACATGAGAGATCTGAGGT 540
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 481 GCCAGGCGATGAGCAAGTGGGCAAGGAGGCGTATCACGCTGAGAGATCAACACC 540
OY 541 ATGCAACAGACACTGAGAGTGGTTGAAGCATGCAATTTGACCGGTGTTACTGCTCA 600
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 541 TTGGGCTGACGCTGAGCTCAGCTCAGCGAGTATGCGGCTTGCACAGGCTCATCTCG 600
OY 601 TACATGCTCAGACATGAAATATGTTGACACCTTGAAGAACCCATTATCTTAATC 660
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 601 TACTTCTGACCGACCGGAGCTCAGAGGAGGCTCTGAGAGACCCCTCATCTGCTG 660
OY 661 ACGATTAATAAAGTCAAAATCAACAGATTTTGCACACTTGAAGAGTCTTAA 720
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 661 GTGAGCTCAAGATGCTCAGTCAAGAGATCTGCTGCTGCTGCTGAGAGGCTATCG 720
OY 721 ACAAACGCTCATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGAT 780
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 721 GCCGAGTAAAGCCCTCTGATCATGCGCGAGAGCTGAGGCGAGGCGCTGTCCACCG 780
OY 781 GCTTGAACAGATTCGTGCTGCTTCAATGATGATGATGATGATGATGATGATGATGAT 840
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 781 GTCTCAACAGATTCGCGGCACTTCAAGTGGTGGGCTCAAGGCTCCCGCTTGGC 840

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Oy	841	GACGTCGTAAAGCTATGCTGTGAAGACATATTCATCTTGGACAGGTGGTACAGTATTACA	900
Dd	841	GACCCGCCAAGCGCATCTTCGACAGGATATGGCCATTCTCCACCGGTGGTATGATCAGC	900
Oy	901	GAGGATCTAGGACTGTAAATTTAAAGATGCTACATGACAGCCCTTGGACAGGCTGTCTAAG	960
Dd	901	GAGGAGGTGGGCGCTCGACGCTGGAGACGCGGACCTGTGCTGTCTAGGACAGGCCCGGAC	960
Oy	961	ATTACAGTTGATTAAGATATGACACAGTAAATGTTGGAAGGTTTACGAAAGTTACAGAGCTATT	1020
Dd	961	GTCTGTGTACACCAAGGACACAGACACCATGTCTGAGGGCGCCGGTGAACCGAGCGCATC	1020
Oy	1021	GCTAAACCTATTGCACTGATTTAAATTCGCAATTTGAAAGAACACATTCTACATTGACCGT	1080
Dd	1021	GCGGACGAGTGGCCCGCATGTCCGCAAGGATGTGAGAACACGCTCGACATGACCGGT	1080
Oy	1081	GAAAACTCACAGAGAGCTTTGGCGAAATTTGCGTGGGTGTACGCTTTTCCAAATAGGA	1140
Dd	1081	GAGAACTGTGCGAGGAGCGCTGTGCCAACGCTGCCGGTGTGTCCGGTATTCAGGCCGGT	1140
Oy	1141	GCTCCACACAGACACACTTTTAAAGAAATGAAACTTCGCAATTGAGATGCTCTTAAATGCT	1200
Dd	1141	GCGCGCACCGAGTGCAGACTCAGAGACGCGAAGCACCCGATTCAGGATCGGTTTCGCAAT	1200
Oy	1201	ACAGTGCAGCCCTTGAAAGAGATATCGTTGCTGTGTGGAGACACACTTATTACGTT	1260
Dd	1201	GCCAAAGCGCCCTGTCAAGAGAGGAGATGTGCCGGTGGGGTGTGACGCTGTTCAGAGCG	1260
Oy	1261	AATGAAAAGATAGCACACTCTTGACACTTGAGGGCGATGTGATGCTACTGACGATTAATGTTG	1320
Dd	1261	GCCCCGACCTTGACAGAGGTATMACTGTGAAGCGAGAGCGACCGGCCACCAATATGTTG	1320
Oy	1321	CTTCGTGCTTAGAAGAGCGCTGTACGCAAAATTCCTTTTAAATCTGGGTACGAAAGGCTCC	1380
Dd	1321	AAGGTGGCGCTGGAGGCCGCCGCTGAACAGATCGCCTTCAACTCCGGGTGGAGCCGGGG	1380
Oy	1381	GTAGTATTATACAAAGTTGAAAAGACGCCGTGAGAGAAAGAGATTTAAATGTCGAAACAGT	1440
Dd	1381	GTGGTGGCCAGAAAGGTGGGCAACTCTCGGGGTGGCCAGCGGATGAAACGCTCAACCGGT	1440
Oy	1441	GAGTGGGTATGTGATTTAAAGACGAATCATTTGACCCCTGTCAAAATGAATACAGATCAAGG	1500
Dd	1441	GTCTACAGAGATATGCTGCGCTCCGCGGCTGTCTGACCCCGGTCAAGGTGACCCGTTGGGG	1500
Oy	1501	CTTCAAAAATGCACTCTTGTAAGCTATCTTATTTTGAACACAGAAAGATGTTGTTAAT	1560
Dd	1501	CTGCAAGAAATGGCGCTCATCTGCGGGGCTGTTCAGACACGAGCGCGTGTTCGCGAG	1560
Oy	1561	AAACCTGAA 1569	
Dd	1561	AAGCCGGAA 1569	

RESULT 10
US-10-267-311-16
: Sequence 16, Application US/10267311
: Publication No. US20030050469A1

```

? LENGTH: 1920
? TYPE: DNA
? ORGANISM: Artificial Sequence
FEATURE:
? OTHER INFORMATION: fusion sequence
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (1... (1917)
US-10-267-311-16

Query Match      28.0%   Score 458.6, DB 9; Length 1920;
Best Local Similarity    55.8%   Pred. NO. 2,8e+102;
                        0; Mismatches 694; Indels 0; Gaps 0;
Conservative

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QY 901 GAGATCTAGACCTGTAATTAAGATCTACATACAGCCCTTGACAGGCTGCTAG 960
    || || || || || || || || || || || || || || || || || || ||
Db 901 GAGAGAGTGGCGCTGACGCTGAGAGAACCGACCTCTGCTGCTAGCAAGCCGCAAG 960
QY 961 ATTAGCTGTAATTAAGATTAAGACATATTTGTAAGTTCAGCAATTCACACCTATT 1020
    || || || || || || || || || || || || || || || || || || ||
Db 961 GTGCTGTACCAAGAGACAGACACCACTGCTGAGAGGCGCGGTGACACCCACCTTC 1020
QY 1021 GCTACACGATTCATGATTAATTCGATTAATTAAGAACCAACACTTCTGACCTT 1080
    || || || || || || || || || || || || || || || || || || ||
Db 1021 GCGGAGAGAGTGGCCGAGATTCGCGCAGAGATGAGAAACAGCAGCTCCAGACACCGT 1080
QY 1081 GAAATCTACAGAACGTTTGGCGAATTAAGCTGTGTGTAGCTTATTAAGATGAGA 1140
    || || || || || || || || || || || || || || || || || || ||
Db 1081 GAGAACCTCTCAGAGAGCGGCTGCAAGCTGCGGTGTGTGTGTGTGTGTGTGTGTGT 1140
QY 1141 GCTCCAGAGAGAGCTTTAAAGAAATGAACCTTGCATTTGAGATGCTGTATATGCT 1200
    || || || || || || || || || || || || || || || || || || ||
Db 1141 GCGGCAACGAGAGTGCAGCTCAAGAGAGCGCAGACCGCATCGAGATCGGGTGGCAT 1200
QY 1201 ACAGTGCAGCGCTTGAAGAGTATCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1260
    || || || || || || || || || || || || || || || || || || ||
Db 1201 GCGCAAGCGCGCGCTGAGAGAGGCGATGCTGCGGCTGTGTGTGTGTGTGTGTGTGTGT 1260
QY 1261 ATGAAAGATGAGACGCTGTGAGGCTGAGGAGATGATGCTAGCTGATCAACCTGTG 1320
    || || || || || || || || || || || || || || || || || || ||
Db 1261 GCGCCAGCCCTGAGAGAGCTGAACTGCAAGGCGAGAGCGGAGCGCCAGCACTGTGTG 1320
QY 1321 CTTCGTGCTAGAGAGCTGTACGTCAAAATGCTTTAAATGCTGGGTAGCAGAGCTCC 1380
    || || || || || || || || || || || || || || || || || || ||
Db 1321 AAGGTGCGCTGAGAGCGCCGCTGAGAGATGCTTTCAACTCGCGGTGAGCGCGGC 1380
QY 1381 GTAGTATTAAGCAAGTTGAAAAAGCCCTGACAGAGACGATTTAATCTGCAACAGT 1440
    || || || || || || || || || || || || || || || || || || ||
Db 1381 GTGTGCGCGGAGAAAGTGGCGCAACCTGCGGCTGAGCGGAGCAAGCACTGACAGCGGT 1440
QY 1441 GAGTGGCTGATATGATTAAGACAGAAATCATTAATGACCTGCAAGTACAGATGAGC 1500
    || || || || || || || || || || || || || || || || || || ||
Db 1441 GTCTAGAGAGATCGCTGCTGCTGCGGCTGCTGAGCGGCTGCAAGGAGTACCGCTTCCGCG 1500
QY 1501 CTTCAAAATGAGCTTCTGAGCTGATGCTTATTTTGAACAGAGAGATGTTGTGCAAT 1560
    || || || || || || || || || || || || || || || || || || ||
Db 1501 CTCAGAAATGCGGCTCATCGCGGCGGTGTCTGTGACCAAGCGCGCTCTCTTCCGAGC 1560
QY 1561 AAGCTGGA 1569
    || || || || ||
Db 1561 AAGCCGGA 1569
    || || || || ||

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OTHER INFORMATION: fusion sequence
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1944)
US-10-267-311-28
Query Match 28.0%; Score 458.6; Db 9; Length 1947;
Best Local Similarity 55.8%; Pred. No. 2,8e-102;
Matches 875; Conservative 0; Mismatches 694; Indels 0; Gaps 0;

QY 1 ATGGCAAAAGAAATCAATTTTACAGCATGCGGCTGCTCCATGTGTGCGCGAGTGTAT 60
    || || || || || || || || || || || || || || || || || || ||
Db 325 ATGGCAAGACATTTGCTAGCAGAGAAAGAGCGCCGTGCGCTGACCGGCGGCTTGAAC 384
QY 61 ATGTACAGATACCGTCAAGTACGCTGTGCTCTTAAGGCGCAATGTTCTTGA 120
    || || || || || || || || || || || || || || || || || || ||
Db 385 GCGCTGCGCATCGGTAAAGTGAATGATGAGGCGCCCAAGGCGCGCAAGCTGTCTGGA 444
QY 121 AAGCTTGTGCTTCCCTTAATTAATGAGGCTGTAACATTTGCTAAAGATGCA 180
    || || || || || || || || || || || || || || || || || || ||
Db 445 AAGAAATGAGGCTGCCCGCAGATCAGCAAGATGATGTGTGTGTGTGTGTGTGTGTGT 504
QY 181 TTAGAAATATTTTGAAGACATGAGCAAAATTTGTGTGTGAAGTGTCTTAAACC 240
    || || || || || || || || || || || || || || || || || || ||
Db 505 CTGAGGATCCGTACGAGAGATGCGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 564
QY 241 AATGATATTTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 300
    || || || || || || || || || || || || || || || || || || ||
Db 565 GATGATCTCCCGGTGAGCGGACAGACGCGCACCGTGTGTGTGTGTGTGTGTGTGTGTGT 624
QY 301 GAAAGACTAAATAATGTGACAGAGTGTCTATCTCAATTTGTATCGTGTGAGCATGAA 360
    || || || || || || || || || || || || || || || || || || ||
Db 625 GAGGCGCTGCGCAAGCTGCGCGCGCGCGCAACCGCTGTGTGTGTGTGTGTGTGTGTGT 684
QY 361 ACAGCAACAGCAACAGCTGTGTGAAGCTTGAAGCAATGCTCAACCTGTATGTGCAAG 420
    || || || || || || || || || || || || || || || || || || ||
Db 685 AAGCGCTGAGAGAGTACCGAGAGACCTGCTGCAAGGCGCGCAAGAGTGTGAGCAAG 744
QY 421 GAGCTATTTCTCAGCTGCTGCAATGATCATCAGCTGTCAAAAGTGTGAGATATAC 480
    || || || || || || || || || || || || || || || || || || ||
Db 745 GAGCAATTTCCGCGCACCGAGATTTTGGCGGCTACCATGATGATGATCTGAGT 804
QY 481 TCAAAATCTGAGACGCTGTGGCAACGATGTGTGTATTCATGTAAGATCTGAGGT 540
    || || || || || || || || || || || || || || || || || || ||
Db 805 GCGGAGCGATGAGCAAGAGTGGCAACGAGGCGCTCATCCGCTGAGAGAGTCAACACC 864
QY 541 ATGGAACAGAACTGAAGTGTGTGAAGCATGCAATTTGACCGTGTACCTGTCTAA 600
    || || || || || || || || || || || || || || || || || || ||
Db 865 TTTGGCTGTGAGCTGAGAGCTACCGAGAGGTATGCGGTTGCAACAGGCTACATCTCGGG 924
QY 601 TACATGCTACAGACATTAAGAAATGTTGACAGCTTGAAGAACCTTATCTTAATC 660
    || || || || || || || || || || || || || || || || || || ||
Db 925 TACTTCTGACGAGACCGGAGCGCTGAGAGCGGTCTCTGAGAGACCTCATCTGCTG 984
QY 661 ACGGATAAAGTGTCAAACTCAAGCAATTTTGCACACTGAGAGAGTCTTAA 720
    || || || || || || || || || || || || || || || || || || ||
Db 985 GTGAGCTCAAGAGTGTCTACGTCAGAGATGCTGCGCTGTGAGAGAGTCACTCGGA 1044
QY 721 ACGAAGCTGCTATTCATTAATGAGATGATGATGATGAGAGCACTTCACACCTT 780
    || || || || || || || || || || || || || || || || || || ||
Db 1045 GCGGTAGAGCTGCTGATCATGCGAGAGAGTGTGAGGCGAGGCGCTGTCAACCTG 1104
QY 781 GTCTTGAACAGATTCGTGTACTTCAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 840
    || || || || || || || || || || || || || || || || || || ||
Db 1105 GTCTCAACAAATCCCGGACCTTCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1164
QY 841 GATGCTGTGAAGTATGCTTGAAGCATTCATCTGTACAGAGTGTGTGTGTGTGTGTGTGT 900
    || || || || || || || || || || || || || || || || || || ||
Db 1165 GAGCGCGCAAGGCGATGCTGAGATATGCGCATTCACCGGTGTGTGTGTGTGTGTGTGT 1224
QY 901 GAGATCTAGACCTGTAATTAAGATGCTCAATGCAAGCGCTTGTGAGAGAGTGTAG 960
    || || || || || || || || || || || || || || || || || || ||
Db 1225 GAAAGAGTGGCGCTGAGCTGAGAGAACCGCACTGTGCTGTGTGTGTGTGTGTGTGTGT 1284

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OY 961 ATTACAGTGTAAAGATAGACAGATATGTTGAGGTTCAAGAAAGTTCAGAGCTATT 1020
    || || || || || || || || || || || || || || || || || || || || ||
DB 1285 GTCTGTGTACCAAGAGAGACACACATCTGCGAGGCGCGGCGGTGACACGACGCTATC 1344
    || || || || || || || || || || || || || || || || || || || || ||
OY 1021 GCTAACCGTATTGACATGATTAATGCAATTAAGAAACAACACTTGTGACTTTGACCGT 1080
    || || || || || || || || || || || || || || || || || || || || ||
DB 1345 GCGGAGAGAGTGGCCCGGAGATCCGCGAGAGATGAGAAACGAGATCTCGACTACGACCT 1404
    || || || || || || || || || || || || || || || || || || || || ||
OY 1081 GAAAGCTACAGAAAGCTTTGGGAAATAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
    || || || || || || || || || || || || || || || || || || || || ||
DB 1405 GAGAACTGACAGAGAGGCTGCGCAAGCTGCGCGGTGTGTGCGGTGTGTGCGGTGTGTGCG 1464
    || || || || || || || || || || || || || || || || || || || || ||
OY 1141 GCTCCACAGACAGCTTTAAAGAAATGAACCTTGCATTTGAGATGCTTAAATGCT 1200
    || || || || || || || || || || || || || || || || || || || || ||
DB 1465 GCGGCGACCGAGGTGAACTCAAGAGCGCAAGCACCGCATGAGAGATGCGGTTCGCAAT 1524
    || || || || || || || || || || || || || || || || || || || || ||
OY 1201 ACAGGTGACCGCTTGAAGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
    || || || || || || || || || || || || || || || || || || || || ||
DB 1525 GCCAAGGCGCGCTGAGAGAGGCGCATGCTGCGGTGCGGTGCTGCTGCTGCTGCTGCTGCT 1584
    || || || || || || || || || || || || || || || || || || || || ||
OY 1261 ATTGAAAAGTAGACGCTTGTGAGCTTGAAGGCGATGATGATGATGATGATGATGATGATG 1320
    || || || || || || || || || || || || || || || || || || || || ||
DB 1585 GCGCGACCGCTGAGAGCTGAGCTGCAAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAG 1644
    || || || || || || || || || || || || || || || || || || || || ||
OY 1321 CTTCGTGCTCTGAAAGAGACCTGAGCTCAATTCCTTAAATGCTGCTGCTGCTGCTGCTGCT 1380
    || || || || || || || || || || || || || || || || || || || || ||
DB 1645 AAGGTGCGCTGAGAGCGCGCTGAGAGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1704
    || || || || || || || || || || || || || || || || || || || || ||
OY 1381 GTAGTATTGACAGTGTGAAGAAACGCGCTGAGAGAGATTTAATGCTGCTGCTGCTGCTGCT 1440
    || || || || || || || || || || || || || || || || || || || || ||
DB 1705 GTGTGCGCGAGAGAGTGGCAACCGCGCTGCGAGCGCTGAGAGCTGAGAGCTGAGAGCTG 1764
    || || || || || || || || || || || || || || || || || || || || ||
OY 1441 GAGTGGTGTGATGATTAAGAAAGAAATCTATGACCGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
    || || || || || || || || || || || || || || || || || || || || ||
DB 1765 GTCTACAGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1824
    || || || || || || || || || || || || || || || || || || || || ||
OY 1501 CTTCAAATGACGCTCTGATGATGCTTATTTTGAACAACAGAAAGTGTGCTGCTGCTGCT 1560
    || || || || || || || || || || || || || || || || || || || || ||
DB 1825 CTGCAAGATGCGGCTCATGCTGCGGGCTGTCTGATCACCAGAGCGCGCTGCTGCTGCTGCT 1884
    || || || || || || || || || || || || || || || || || || || || ||
OY 1561 AAACCTGAA 1569
    || || || || || || || || || || || || || || || || || || || || ||
DB 1885 AAGCCGAA 1893
    || || || || || || || || || || || || || || || || || || || || ||
```

```
RESULT 12
US-10-267-311-20
: Sequence 20, Application US/10267311
: Publication No. US20030050469A1
: GENERAL INFORMATION:
: APPLICANT: Siegel, Marvin
: APPLICANT: Chu, N. Randall
: APPLICANT: Mizeen, Lee A.
: TITLE OF INVENTION: INDUCTION OF A THI-LIKE RESPONSE IN VITRO
: FILE REFERENCE: 12071/002001
: CURRENT APPLICATION NUMBER: US/10/267,311
: PRIOR APPLICATION NUMBER: US/09/613,303
: PRIOR FILING DATE: 2000-07-10
: PRIOR APPLICATION NUMBER: US 60/143,757
: PRIOR FILING DATE: 1999-07-08
: NUMBER OF SEQ ID NOS: 55
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 20
: LENGTH: 2847
: TYPE: DNA
: ORGANISM: Artificial sequence
: FEATURE:
: OTHER INFORMATION: fusion sequence
: NAME/KEY: CDS
: LOCATION: (1)...(2844)
```

```
US-10-267-311-20
Query Match 28 0% Score 458.6; DB 9; Length 2847;
Best Local Similarity 55.8%; Pied. No. 3,46-102;
Matches 875; Conservative 0; Mismatches 694; Indels 0; Gaps 0;

OY 1 ATGCGAAGAAATCAATTTTACAGCATGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60
    || || || || || || || || || || || || || || || || || || || || ||
DB 61 ATGCGAAGAAATCAATTTTACAGCATGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
    || || || || || || || || || || || || || || || || || || || || ||
OY 61 ATGTTAGCATACGCTCAAGTAACGCTTGTCTTAAAGGCGCAATGTTCTTTGAA 120
    || || || || || || || || || || || || || || || || || || || || ||
DB 121 GCGCTCGCGGATGCGGTAAAGTGCATTTGGCCCAAGGCGCGCATGCTGCTGCTGCTGCTGCTGCT 180
    || || || || || || || || || || || || || || || || || || || || ||
OY 121 AAGCTTTTGGTCTCTCTTAATTACTTAATGACGGGGTAAACCATTTGTAAGATGCA 180
    || || || || || || || || || || || || || || || || || || || || ||
DB 181 AAGAGTGGGTGCGCCCGACGATCACCAGATGATGATGATGATGATGATGATGATGATGATGATG 240
    || || || || || || || || || || || || || || || || || || || || ||
OY 181 TTGAGAGATCATTTTGAAGACATGAGCAAAATTTGCTGATGATGCTTAAAGAC 240
    || || || || || || || || || || || || || || || || || || || || ||
DB 241 CTGAGAGATTCGATGAGAGATGCGCGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
    || || || || || || || || || || || || || || || || || || || || ||
OY 241 AATGATATTGCTGATGAGGAGACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
    || || || || || || || || || || || || || || || || || || || || ||
DB 301 GATGACGTGCGGTGACGAGCACGAGAGCGCACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
    || || || || || || || || || || || || || || || || || || || || ||
OY 301 GAAGCATTAAGAAATGTGACAGAGTGTAAATTCATTTGATGCTGAGAGCATGAA 360
    || || || || || || || || || || || || || || || || || || || || ||
DB 361 GAGGCGCTGCGCAAGCTGCGCGCGCGCAACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
    || || || || || || || || || || || || || || || || || || || || ||
OY 361 ACAGCAACAGCAACAGCTGTTGAAGCCTTGAAGGCAATGCTCAACCTGATCTGCAAG 420
    || || || || || || || || || || || || || || || || || || || || ||
DB 421 AAGGCGGTGAGAGAGGTCAACCGAGACCTGCTCAAGGCGCCCAAGAGCTGAGAGCATG 480
    || || || || || || || || || || || || || || || || || || || || ||
OY 421 GAAGTATTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
    || || || || || || || || || || || || || || || || || || || || ||
DB 481 GAGCGATGCTGCGCGCACCGCATTTTGGCGGTGACAGCATGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
    || || || || || || || || || || || || || || || || || || || || ||
OY 481 TAGAAGCATGAGAGCGTGTGGGCAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
    || || || || || || || || || || || || || || || || || || || || ||
DB 541 GCGAGGCGATGACAGAGTGGGCAAGGCGCTGATCAACGCTGATGATGATGATGATGATGATGATG 600
    || || || || || || || || || || || || || || || || || || || || ||
OY 541 ATGGAAGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
    || || || || || || || || || || || || || || || || || || || || ||
DB 601 TTGCGGTGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
    || || || || || || || || || || || || || || || || || || || || ||
OY 601 TACATGCTGACAGACATGAGAAATGCTTGAAGACCTTGAAGACCTTGAATATC 660
    || || || || || || || || || || || || || || || || || || || || ||
DB 661 TACATGCTGACAGACATGAGAAATGCTTGAAGACCTTGAAGACCTTGAATATC 720
    || || || || || || || || || || || || || || || || || || || || ||
OY 661 ACGATTAAGAAATGCTCAAGATGCAAGACATTTTGGCACTGATGAGAGATCTTAA 720
    || || || || || || || || || || || || || || || || || || || || ||
DB 721 GTCACTTCAGAGTGTCACTGCAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
    || || || || || || || || || || || || || || || || || || || || ||
OY 721 ACCAAGCTCATTAATCATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
    || || || || || || || || || || || || || || || || || || || || ||
DB 781 GCGGTGAAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
    || || || || || || || || || || || || || || || || || || || || ||
OY 781 GCTTGAAGCAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
    || || || || || || || || || || || || || || || || || || || || ||
DB 841 GTCTGCAAGATGCGCGGACCTTCAAGTGTGGGCGGTGCAAGGCTTCCGCGCT 900
    || || || || || || || || || || || || || || || || || || || || ||
OY 841 GATGCTGTAAGCATGCTGTAAGCATGCTGTAAGCATGCTGTAAGCATGCTGTAAGCATGCTGTAAG 900
    || || || || || || || || || || || || || || || || || || || || ||
DB 901 GACCGCGCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
    || || || || || || || || || || || || || || || || || || || || ||
OY 901 GAGATCTAGAGCTTGAATTAAGATGCTGATGATGATGATGATGATGATGATGATGATGATGATG 960
    || || || || || || || || || || || || || || || || || || || || ||
DB 961 GAGAGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGT 1020
    || || || || || || || || || || || || || || || || || || || || ||
OY 961 ATTACAGTGTAAAGATAGACAGATATGTTGAGGTTCAAGAAAGTTCAGAGCTATT 1020
    || || || || || || || || || || || || || || || || || || || || ||
DB 1021 GTCTGTGTACCAAGAGAGACACACATCTGCGAGGCGCGGCGGTGACACGACGCTATC 1080
    || || || || || || || || || || || || || || || || || || || || ||
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US-09-738-626-2986
 Query Match 27.9%; Score 457; DB 9; Length 1644;
 Best local similarity 56.4%; Pred. No. 6, 4e-102;
 Matches 903; Conservative 0; Mismatches 680; Indels 18; Gaps 2

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OY 1 ATGCCAAATAAATCAATTTTTCAGACAGATGCGGTGCTGCCATGTGCCGAGTGTAT 60
DB 1 ATGCCAAAGATCATCGCTTTTGATGAGAGAGACGTGTGTCCTGAAAAGGAGACTGAC 60
OY 61 ATGTTACAGATACCGTCAAGTAACGCTTGCTCTAAAGGCGCAATGTTGTTTGAA 120
DB 61 ACCCTGCTACGCGTGTAAAGGTAATTTGGAGACCAAAAGGCGCGTAACGTCGTTTGGAA 120
OY 121 AAAGCTTTGGTCTCCCTTAATTAATAAGCGGGTAACCATGCTTAAGAGATCGNA 180
DB 121 AAAGCTTTGGGTGCCCCACCACTTTTACCACAGATGTGTACCATTGCAACGTGTAGAG 180
OY 181 TTAGAGATCATTTTGAACACATGGAGGAGCAAAATTTGGTGTCTGAAGTGGCTTTAAACC 240
DB 181 CTTAGAGATCTTACGAAAGAGATCGGCGGACAGCTGATGTCAGAAAGTGTGCTTAAGAACT 240
OY 241 AATGATTTTCTGTGATGGAGAGACTACTGACATATTTTACCAAGCAATGTTCAT 300
DB 241 GATGACCTCGCGGGGATGGACACCAACCGCTACGTAATTTGGCAAGGCTGTGTTGG 300
OY 301 GAAGACTTAAATAATGTGACAGAGGCTGTAAATCCATTTGATATCGTACAGGCAATGA 360
DB 301 GAAGCGCTCGCAAGCTTGTCTGTGCTGTATACCCATTTGGCATTAACGCTGGCATCGAG 360
OY 361 ACACACACAGCAACGCTGTGTGAAGCTGTGAAGCCATTGCTCAACCTGTATCTGGCAAG 420
DB 361 AAGGCTTTGCTCAAGTAACGTACTGAGAAAGCTGCTGAGGCTGGCAAGAAATTGAGACGAG 420
OY 421 GAACCTTTTGTCTCAAGTGCCTGCGATGATCATACGCTCTGAAAAGTTGGAGAGTAATTC 480
DB 421 GAGCAGATGCTGCTTACCGCTGTGATTCGCGAGTACCCACGATTCGGCGGACAGATT 480
OY 481 TCAGAACCTATGGAACGTGTGGG-----CAAGATGATGTGATTACATC 535
DB 481 GCTAAGGCAATATACGAGATGTGGCGGTGGCAAGCTGACAGACAGATTCCTCGATCACTCTT 540
OY 546 GAAGAACTTCGAGGATGTGAACACAGAACTTGAAGTGTGAAGCATGCAATTTACCGT 585
DB 546 GAAGAGTCACACACTTCCTGGGTGTGGTGTGAGCTTACGAGGTAATGCCCTTTGATTAAG 600
OY 586 GGTATCCTGTCTCAATACATGTGTCACACACATGTAAGAAATAGTTGTCAGACCTTGAAC 645
DB 601 GGCTACATCTCGGTTACTCTTCGCACTACATGAGACGCGCTGAGGCTGTTCGGAAT 660
OY 646 CCATTTCATTATACAGGATTAATAAATGTGCAACATCAAGACATTTTGGCACTACTT 705
DB 661 CCTTACATCTCTGCTGTTCGCGGCAAGATCTCCACATCAAGAGCTGCTCCCACTGCTG 720
OY 706 GAGGAGTTCTTAAACCAACGCGCTCATTTCTGATTTATGAGAGATGATGATGATGATGA 765
DB 721 GAGAAAGTATCAGATCCGCGCAAGCCTTGTGTATCTATCTCGAGAGACGTCCAGGGCGAG 780
OY 766 GCACTTCACACCTGTCTGAAACAAGATTCGTGTGATCTTCAATGTGTGCTGTCAA 825
DB 781 GCTGTGTCACCTGTGTGTGTAACCAAGATTCGTGTGAGCACTTCCTTAAGTGTGTCTTTAAG 840
OY 826 GCGCCAGGATTTGGTATCGTGTGAACCTATGCTGAAGACATTTGCTATCTTGACAGT 885
DB 841 GCTCCGGGCTTGCGCGACGCTGTGAAGGCTCCTACCTCAGACGACATTTGCTGTTCGCGGT 900
OY 886 GGTACAGTATTACAGAGATCTAGGACTTGAATTTAAAGATGCTACATGACACCCCTT 945
DB 901 GGCCAGGTATTTCTGAAGAGGTGGCTCTCCCTTGAGACCGCTGTATCGCACTTCTA 960
OY 946 GGACAGGCTGCTAGATTAACTGATTAAGAGATGACAGTAATTTGTGAAGCTTCAGGA 1005
DB 961 GGCCAGGCGCAGAGGTTGTGTCTACCAAGAGATGACACACCATCTGTTGAGCGGCGAGT 1020
  
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Wed Apr 16 08:05:37 2003

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Page 14

Oy	1006	AGTTGACAAAGCTATTGCTAAACCGTATTGACATGATTAAATTCGCAATTGTGAACAAACAAC	1066
Db	1021	TCGAGGGCTCAGATTCAGAAAGGCGCGGTCAACCAAGATCCCGCTGAGATGAGAAATCCGAT	1080
Oy	1066	TCTGACTTTGACCGTGAACAAATCAACAAGACGTTTGGGAAATTAAGTGGTGATAGT	11255
Db	1081	TCGCGACTCGACGCTGAGAAAGCTCAAGACCGCTGCGCTAAGCTTGGCGGCGGTTTGA	1140
Oy	1126	GTTATCAAAAGTAGSAGCTCCAAACAGACAGCTTTAAATAAATGAATTCGATTTAG	1185
Db	1141	GTCCTTAAGTGGGGCCACACTACCGAGGTTGAGCTCAAGAGAGCCCAAGACCGGATTTAG	1200
Oy	1186	GATGCTCAAAATGCTACACGTGACGCCGTTGAAGAAGTATCTGTGCTGGTGTGACAA	1245
Db	1201	GATGCTGCTCGTAACCTTAAGCAGACGTTGTGAAGAGGCAATCGTCGGCGGCTGGCCGTT	1260
Oy	1246	GCACTTATTACGTTATTGAAAAAGT---CAGCTCTTGAAGCTGAAGCGATGATGT	1302
Db	1261	GGCGTCTGCAAGGCTCTCTACGTCCTGAGCAACGATCTTAGCTTCCGGAGCAGAGGA	1320
Oy	1303	ACTGAGACGTAACTTTGTGCTCTGAGCTTGAAGAGACGCTGACGTAAATTCGTTAAAT	1362
Db	1321	ACCGGCGTTGTCATCTCTCCGGAGGCTCTGACGTGCTCTGTGAACAGATGCTGTATAC	1380
Oy	1363	GCTGGGTACGAAGGCTCGTATGATTATGCAAGTTGAAGAAACAGCCGCGAGAACAGGA	1422
Db	1381	GCTGGCTCCAGCCAGCGGTTGTGTGACAAAGTTTCCCACTCCCAACAGCCGAGGCGC	1440
Oy	1423	TTTATGTCACAAAGGATGATGAGTGTGAATGATTTAAACAGAGATCATTCACCTGTG	1482
Db	1441	CTCAACGCTGCAAAAGCGGAGATAGTCACTCACTCAGTCTGCGGAGATCAACGACGAGT	1500
Oy	1483	AAAGTAACAGACGACGCCCTTCAAAAATGCAAGCTCTGTGATAGTCTTATTTTGAACAA	1542
Db	1501	AAAGTCAACCGGCTCGCACTCCAGAAACGCTGCATCCATTCGACAGCTCTGTCTCGACACT	1560
Oy	1543	GAGCAGTGTGTTCTTAATTAACCTGAACAGCTACGCGAGC	1583
Db	1561	GAGGCTGCTGTCTGCAACAAACGCTCAGCGCCAGCGCAGC	1601

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RESULT 14
US-09-738-626-1/c
Sequence 1, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAMA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OGHTAI, KEIICHI
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, MAKOTO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASARU
APPLICANT: OZAWA, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738, 626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PatentIn ver. 3.0
LENGTH: 309400
SEQ ID NO 1
TYPE: DNA
ORGANISM: Corynebacterium glutamicum

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US-09-738-626-1

Query Match	27.9%;	Score 457;	DB 9;	Length 3309400;
Best Local Similarity	56.4%;	Pred. No. 3.4e-100;		
Matches 903;	Conservative	0;	Mismatches 680;	Indels 18; Gaps 2

[illegible]

Db	454	GCCAAAGCAATTTGGCGTACGACGAAGAGGCCGCTCGGGGCTCGAGACCGGGCTTGAAACCC	513
OY	64	TTACAGAGATACCGTCAATAAGTACGGTGTCTCTAAAGGGGCGAATGTTGTCTTGAAAA	123
Db	514	CTCGCGATGGCGGTAAAGTGATTTGGGCCCAAGGCCGACAGCTGCTCTGGAAAAG	573
OY	124	GCTTTGGTCTCCCTTAATTTCAATATAGGGGGTAAACATGCTTAAAGATTCGAATTA	18
Db	574	AAGTGGGGTCCCCACAGATCAACACATATGTGTCTCATTCGCAAGAGATCGAGCTG	63
OY	184	GAGATTCATTTGAAACATATGGAGACAAATTTGGTCTCGAAGTGGCTTTAAACCAAT	243
Db	634	GAGGATTCCTTAGAAGAAAGATTCGGCGCGACCTGGTCAAAAGAGTGGCAAGAAAGCCAT	693
OY	244	GATTTTGGTGGTATGGAGACACTCTGCACAGTTTTGACACAGCCATTTGTCATGAA	30
Db	694	GAGCTGGCGGGGAGCGACACAGAGGCCCTGCTGGCCGAGGGGTGGTGGCAG	753
OY	304	GGACTTAAATAATGTGACAGAGGCTCTAATCCAAATTTGATTCCTCGAGGCAATTGAACA	36
Db	754	GGCCTCGCAGACGTGCGGGCGGGCCGACCCGCTGGGTCTCAACCGCGCATCGAAAG	813
OY	364	GCAACGACAGACGCTGTGAAGCCCTTGAAAGCCATTGGCTCAACCTGTATCTGGCAAGAA	423
Db	814	GCGCTGGAGAAAGGTGCACACGACACCTGTCTAAAGGGCGCCAAAGAGGTGCGAGCAAGAG	873
OY	424	GCTATTGCTCAGGTGCGTCAATATATCAACGCTCGAAAAAGTTGAGAGTATCTCA	483
Db	874	CAGATTGGCGCACCGGACCGACGATTTTCGGCGGGTACAGATCCATTCGGTGCATGCGC	933
OY	484	GAGGCTATGAGAGCTGTGGGCGAAGATGTGTATTAACATTCGAAAGATCTCGAGATG	543
Db	934	GAGGGATGTGACAAAGGTGGGCAAGAGGGGCTATCACGCTCGAGAGTCTCAACACCTT	993
OY	544	GAAACAGAACTTGAAGGGTTGAAGGGATGCAATTTGACCGTGTACTGCTCATAC	603
Db	994	GGGCTGACGTGCGAGCTCAACGAGATATCGGTTTCGACAAAGGGCTATCTCGGGTAC	105
OY	604	ATGGTCACAGCAATBAAAAATGGTTCGAGACCTTGAAAAACCATTTATCTAATCAG	663
Db	1054	TTGCTGACCCAGCCCGGAGGCTGAGBAGGCGTCTCGAGAGCCCTCACTTCCTGTGTGTC	111
OY	664	GATBAAAAAGTGTCAACATCTCAAGACATTTTGCACACTTGTGAGAAATTTTAAACC	723
Db	1114	AGCTCCAAAGGTGTCTCTGTCAMAGATCTGTGCGCTGCTCGAAGATCATGGAGCC	117
OY	724	AACCGTCAATTACTATTATTGACAGATGATGTGATGGTGAACACTTTCACACCTTGTG	783
Db	1174	GGTAGCGCGGTGTATCTATCGCCGAGAGAGCTCGAGGGCGAGCGCTGTCCACCTGTGTC	123
OY	784	TTGAACAAGATTTGTTGTAATTCATTAAGTGGTGTCTGTGCAACGCGCAGATATTGGAT	843
Db	1234	GTCAACAAGATTCGCGGCACTTCAATCGTGGTGGCGGTCAAGGCTCCGGGCTTGGGAGC	129
OY	844	CGTCTAAACCTATGCTTGAAGACATTTGCTATCTTGAAGAGTGTACAGTATTAACAG	903
Db	1294	CCCGCAGAGCGATGCTGACGATATATGGCCATTTCAACGCGTGTGTCAGTATATAGCA	135
OY	904	GATTCAGACTTGAATTTAAAGATGCTACAAATGAGACGCTTGGACAGGCTGTAAAGTT	963
Db	1354	GAGGTGGCGCTGACGCTGGAAACGCCGACCTGTGCTGTACGACAAAGCCCCGCAAGGTC	1413
OY	964	ACAGTGTATTAAGATATAGACAGTATTTTGAAGTTCAAGAGTTCAAGATTTGCT	1023
Db	1414	GTGGTCAKAGAGACAGAACACCATCTGTCGAGGGCCGCTGTACACCGAGCCATCTGCC	1473
OY	1024	AACCGTTATTCACATTAATTAATGCAATTAAGAACAAACAATTTGACTTTGACCTGAA	1083
Db	1474	GGAGCAAGTGGCCCAATCCGACAGGAGATCGAAGACAGCACTCGACTACAGACCTGTAG	1533
OY	1084	AACCTACAAAGACGTTTGGGAAATTTAGCTGTTGCTGTATGCTATTATTAAGATAGAGCT	1143

Db 1534 AACCTCAGAGAGCGGCTGGCCAAAGCTGGCCGGTGTGTCCGGTATCAAGGCCGCTGCC 1593
OY 1144 CCAACAGAGACAGCTTTAAAGAAATGAACCTTCCGATTGAGATGCTCTAAATCTACA 1203
Db 1594 GCCACCGAGGTCAACCTCAAGAGAGCCCAAGCACCCTCATCGAGATGGGTTGCCAATGCC 1653
OY 1204 CGTGAAGCCGTTGAAGAGCTACCTGCTGTGTGTGAGACAGCATTATTAAGGTTATT 1263
Db 1654 AAGCCGCCCTCGAGAGGCAATCGTCCGTGGGGGTGTACGCTGTTCAGACCGGCC 1713
OY 1264 GAAAAAGTACAGCTCTTGAGCTTGAGGGCGATGATGCTACTGAGCCTAAACATTGTGCTT 1323
Db 1714 CCGACCTGAGAGCTGAAGCTCGAAGGCGAGAGCGACCGGCCCAACATCCTGAAG 1773
OY 1324 CGTCTCTAGAGAGCCTGTACGTCAATTTCTTTAAATGCTGGGTACGAAGGCTCCGTA 1383
Db 1774 GTGGCGCTGGAGGCCCGCTGAAGCAGATCGCTTCAACTCCGGGCTGGAGCCGGGCGTG 1833
OY 1384 GTTATTGACAAAGTTGAAAAACAGCCCTGCAGAGACAGATTAAATGCTGCAACAGGTGAG 1443
Db 1834 GTGGCCGAGAGGTGCGCAACCTGCGGCTGGCCAGCGACTGAAAGCTCAGACGGGTGTC 1893
OY 1444 TGGGTTGATATGATTAAACAGAAATCATTGACCCCTGTCAAGTAACAGATCAGCGCTT 1503
Db 1894 TAGAGAGATTGCTCGCTGCGGGGTGTGTAACCGGTCAAGTGAACCCGTTGCGGCTG 1953
OY 1504 CAAAATGCAAGTTCTGTAGCTATGCTTATTTGACACAGAAAGATTGTTCTATATAA 1563
Db 1954 CAGATGCGGGTGCATCGCGGGGCTGTTCTTACACCGAGGCGTGTGCGACAG 2013
OY 1564 CCTGAA 1569
Db 2014 CCGGAA 2019

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Job time : 3195.29 secs